

Figure 1

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Figure 2

1. b. spp1	-----MAASSGCDIAPASSSSPF-----	-----TAASTMSSTFDL-----	-----LA5DAYCCSV-----	43
L. e. byp	KGCGFDRAVINGDIFPSSPFKTFYSSLLDODGGSFLSTPQHTE-----	-----CHLASCQFQEVCH-----		53
L. e. byp	KGCGFDRAVINGDIFPSSPFKTFYSSLLDODGGSFLSTPQHTE-----	-----CHLASCQFQEVCH-----		53
W. t. wky	KGCGFDRAVINGDIFPSSPFKTFYSSLLDODGGSFLSTPQHTE-----	-----CHLASCQFQEVCH-----		53
A. t. put	-----	-----	-----	50
A. t. unk	-----	-----	-----	50
R. c. d-l	-----	-----	-----	50
A. t. byp	-----	-----	-----	50
A. t. wky20	-----	-----	-----	50

I. b. <i>csf1</i>	SEGLG	SEGLGKTCVSPKPSLTPPLS	73
I. e. <i>hyp</i>	SGCDTAPAALEIFPQFVLSVFSQKQDLSKGGCLL	SGCDTAPAALEIFPQFVLSVFSQKQDLSKGGCLL	119
I. e. <i>wky</i>	SGCDTAPAALEIFPQFVLSVFSQKQDLSKGGCLL	SGCDTAPAALEIFPQFVLSVFSQKQDLSKGGCLL	119
I. t. <i>put</i>	SDQADQADATTYK	SDQADQADATTYK	109
A. b. <i>usk</i>	-----	-----	-----
A. c. <i>d-l</i>	-----	-----	-----
A. t. <i>hyp</i>	-----	-----	-----
A. t. <i>wky10</i>	-----	-----	-----
H. v. <i>SV51B1A2</i>	-----	-----	-----

I. b. spp1	SPAVEDSTIPAPFGLSPVLLNSPV1-15-5H	1-15PSPIV1-15-5H	119
I. b. hyp	QNGCVRSPV1-15-5HSPV1-15-5H	VPSPIV1-15-5H	165
I. b. hyp	QNGCVRSPV1-15-5HSPV1-15-5H	VPSPIV1-15-5H	165
N. t. wrky	QNGCVRSPV1-15-5HSPV1-15-5H	VPSPIV1-15-5H	165
A. t. pat	-----	1-15PSPIV1-15-5H	17
A. t. unk	-----	1-15PSPIV1-15-5H	17
R. t. d-1	-----	1-15PSPIV1-15-5H	17
A. t. hyp	ELTVEFRE1-15-5HSPV1-15-5H	VPSPIV1-15-5H	103
A. t. wrky10	ELTVEFRE1-15-5HSPV1-15-5H	VPSPIV1-15-5H	83
E. v. wrky12	ELTVEFRE1-15-5HSPV1-15-5H	VPSPIV1-15-5H	83

I. b. spp1	FRT1	MEASAGQDVFQ	---GKQFDFKQIYQNSG	G	G	162
I. b. hyp	G10N	MEASAGQDVFQ	---GKQFDFKQIYQNSG	G	Y	217
I. b. brp	G10N	MEASAGQDVFQ	---GKQFDFKQIYQNSG	G	Y	217
I. b. wcky	G10S	MEASAGQDVFQ	---GKQFDFKQIYQNSG	G	Y	204
I. a. put	FRT1	MEASG	---GKQFDFKQIYQNSG	G	Y	204
I. a. wck	G10N	MEASG	---GKQFDFKQIYQNSG	G	Y	65
I. a. d-1	G10N	MEASG	---GKQFDFKQIYQNSG	G	Y	65
A. C. hyp	G10N	MEASG	---GKQFDFKQIYQNSG	G	Y	69
A. C. wcky20	G10N	MEASG	---GKQFDFKQIYQNSG	G	Y	151
M. v. SUS182	G10N	MEASG	---GKQFDFKQIYQNSG	G	Y	137

B. 1. sepl	GGTCTTCTCCCT	TTTTC	GGG	TTT	212
B. 1. bryp	GGVTLDSRQVYVQGAAQVQFQDNE	GGPDPDGGCGGDNVAGAGCAGG	GGG	TTT	212
B. 1. bryp	GGVTLDSRQVYVQGAAQVQFQDNE	GGPDPDGGCGGDNVAGAGCAGG	GGG	TTT	212
B. 1. wcky	GGTCTTCTCCCT	GGG	TTT	TTT	212
A. 1. put	GGATGTTGCGGCGGCGGCGGCGGCGG	TTTGGGTTTGGGTTTGGGTTTGGG	TTT	TTT	161
A. 1. wck	GGATGTTGCGGCGGCGGCGGCGGCGG	TTTGGGTTTGGGTTTGGGTTTGGG	TTT	TTT	161
R. 1. d-1	GG-ATG-TGG-TGG-TGG-TGG-TGG	TTT-GAT-TAT-TAT-TAT-TAT	TTT	TTT	141
A. 1. bry	GGGGGGGGGGGGGGGGGGGGGGGGGG	TTTGGGGGGGGGGGGGGGGGGGGGG	TTT	TTT	227
A. 1. wcky2	GGGGGGGGGGGGGGGGGGGGGGGGGG	TTTGGGGGGGGGGGGGGGGGGGGGG	TTT	TTT	227
E. v. sus182	GGAGGGGGGGGGGGGGGGGGGGGGGG	TTTGGGGGGGGGGGGGGGGGGGGGG	TTT	TTT	191

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L. b. bpr VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
L. e. bpr VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
H. t. wcky VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
A. t. put VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
A. t. usk VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
H. t. d-1 VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
A. t. bpr VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
A. t. wcky20 VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK
H. v. SUSI28 VASVARTCQSYRVSKECSEPPRSVYKCHPCKRHHVLLCNSQDCTT176VVKGK

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2. b. <i>SPPI</i>	QKNEESQEVAGGIVVAVREFRVRVVIQITSPIDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
2. e. <i>byp</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
3. e. <i>byp</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
4. e. <i>wcky</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
5. e. <i>pet</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
6. e. <i>esk</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
7. e. <i>d-i</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
8. e. <i>byp</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
9. e. <i>wcky2</i>	RKETCTTCAQGIVVAVREFRVRVVIQITSEVDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31
10. v. <i>SUS181</i>	QKNEESQEVAGGIVVAVREFRVRVVIQITSPIDILQDGCVVAKKQGKTVVQGHPHPFSVYK	31

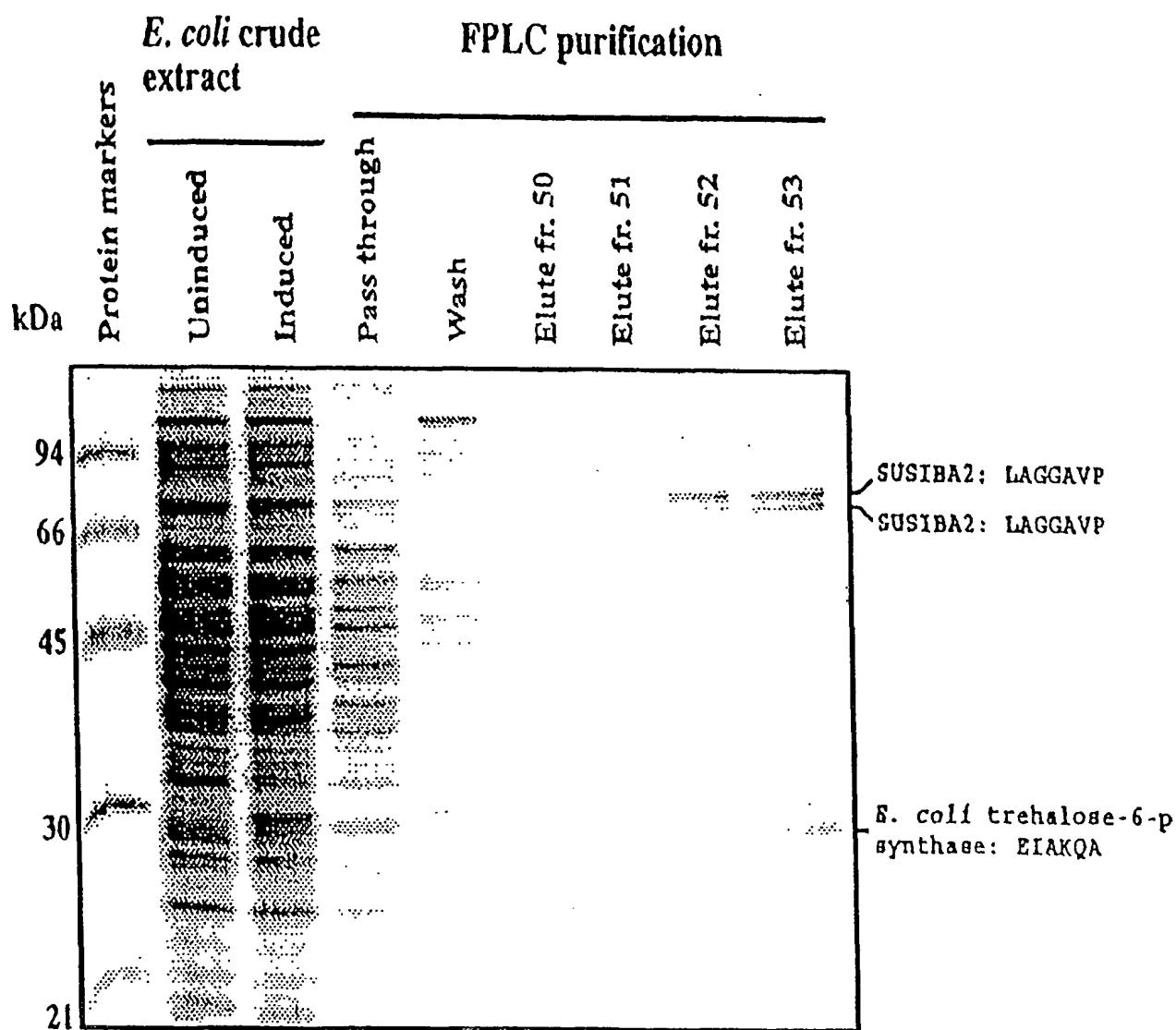
I. b. SP1	RDD-----	ISDNTA-----	545
L. e. bry	KVPEFLSDP-----	GPTATKQFQNSLHGFPR-----	733
L. e. bry	KVPEFLSDP-----	GTTATKQFQNSLHGFPR-----	733
M. t. wrcky	KAEFLMGSQFLDLSNGSXXTQD-----	SGTFLGEG-----	727
A. t. unk	-----	HIGVAF-----	685
A. t. unk	-----	IGAAGSG-----	685
R. r. d-l	-----	KGIVLGF-----	685
A. t. bry	-----	HIGVAF-----	577
A. t. wrcky10	-----	HIGVAF-----	557
M. t. SUS182	-----	IGVAF-----	577

Red

Pink

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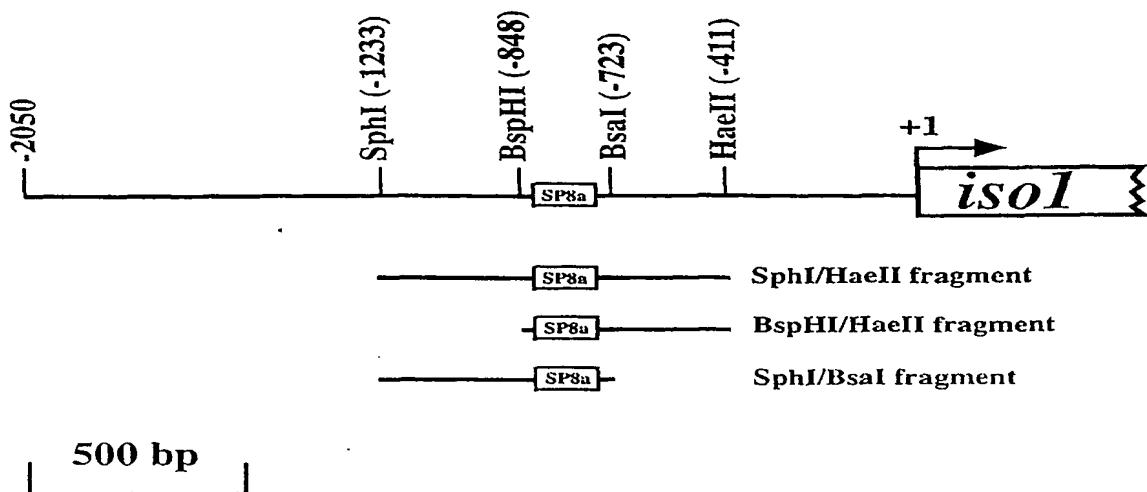
Figure 3

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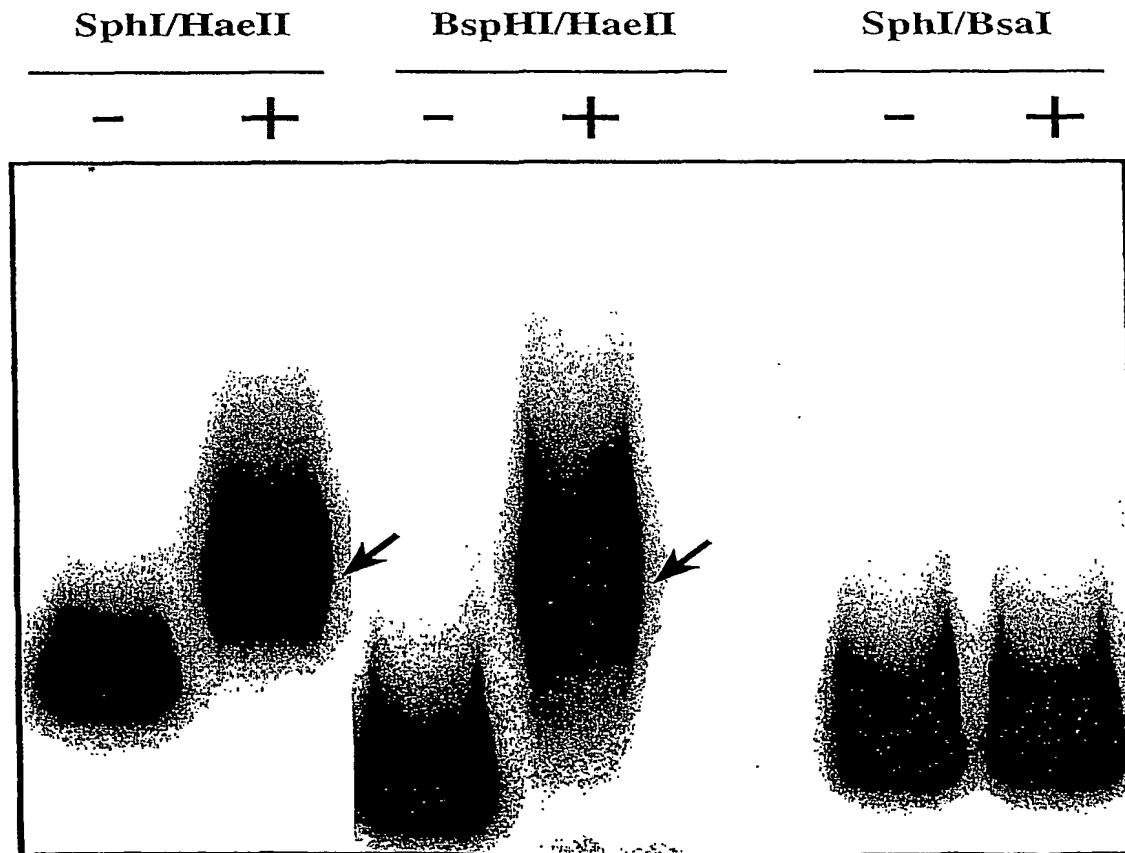
Figure 4

A

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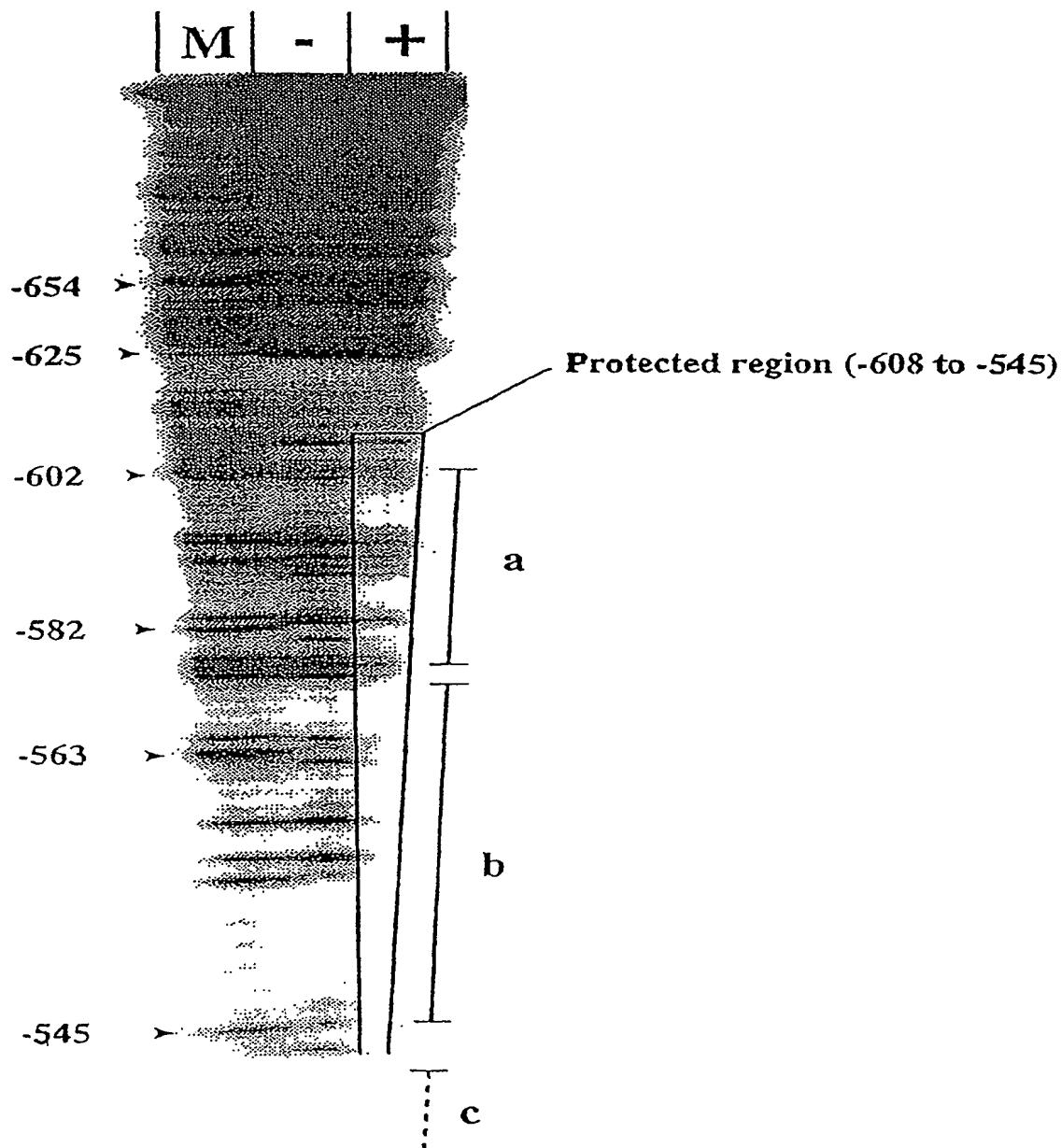


B



A

Figure 5

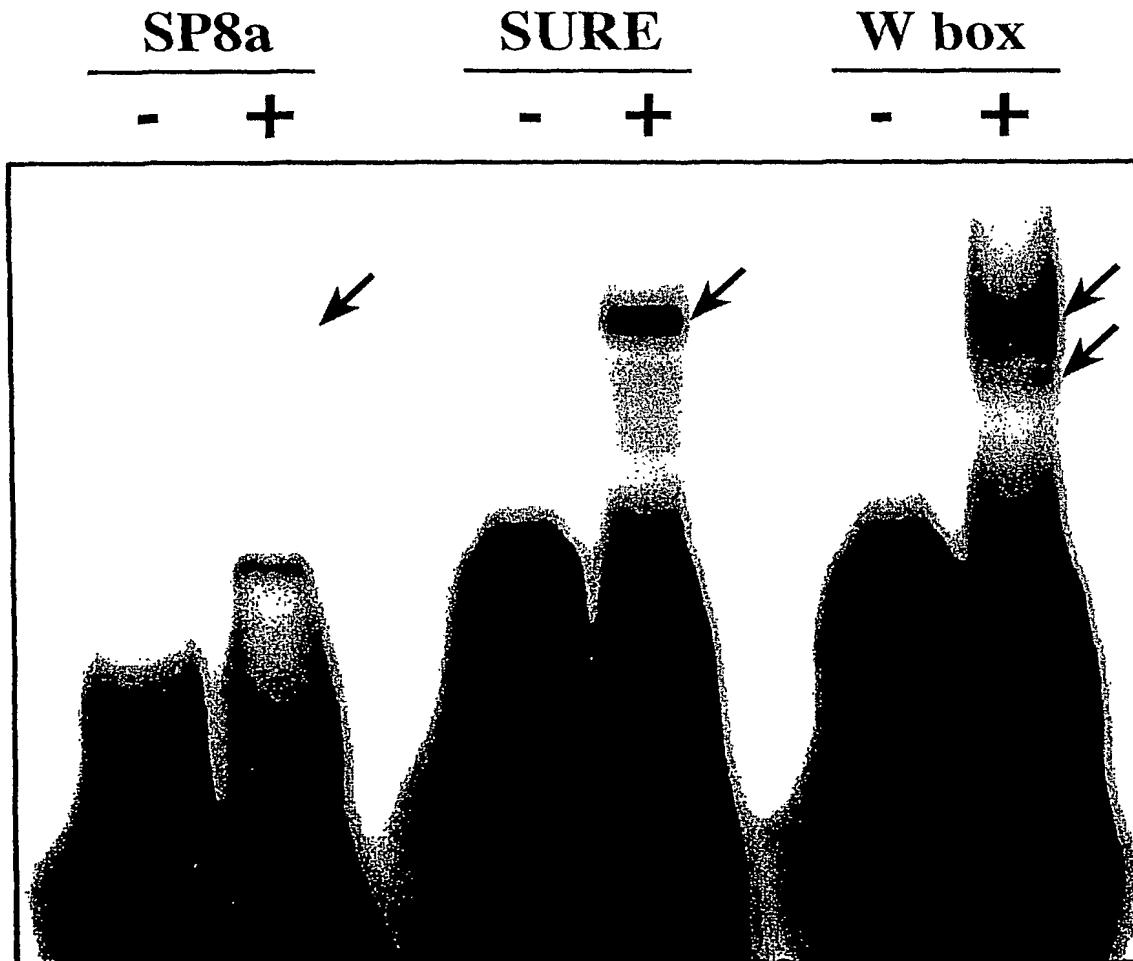


Protected region -568 AATAACCAAAAAATAATAATAAAA -545
Patatin SURE sequence AATAACTAATAAAGAATAGAAAAAA

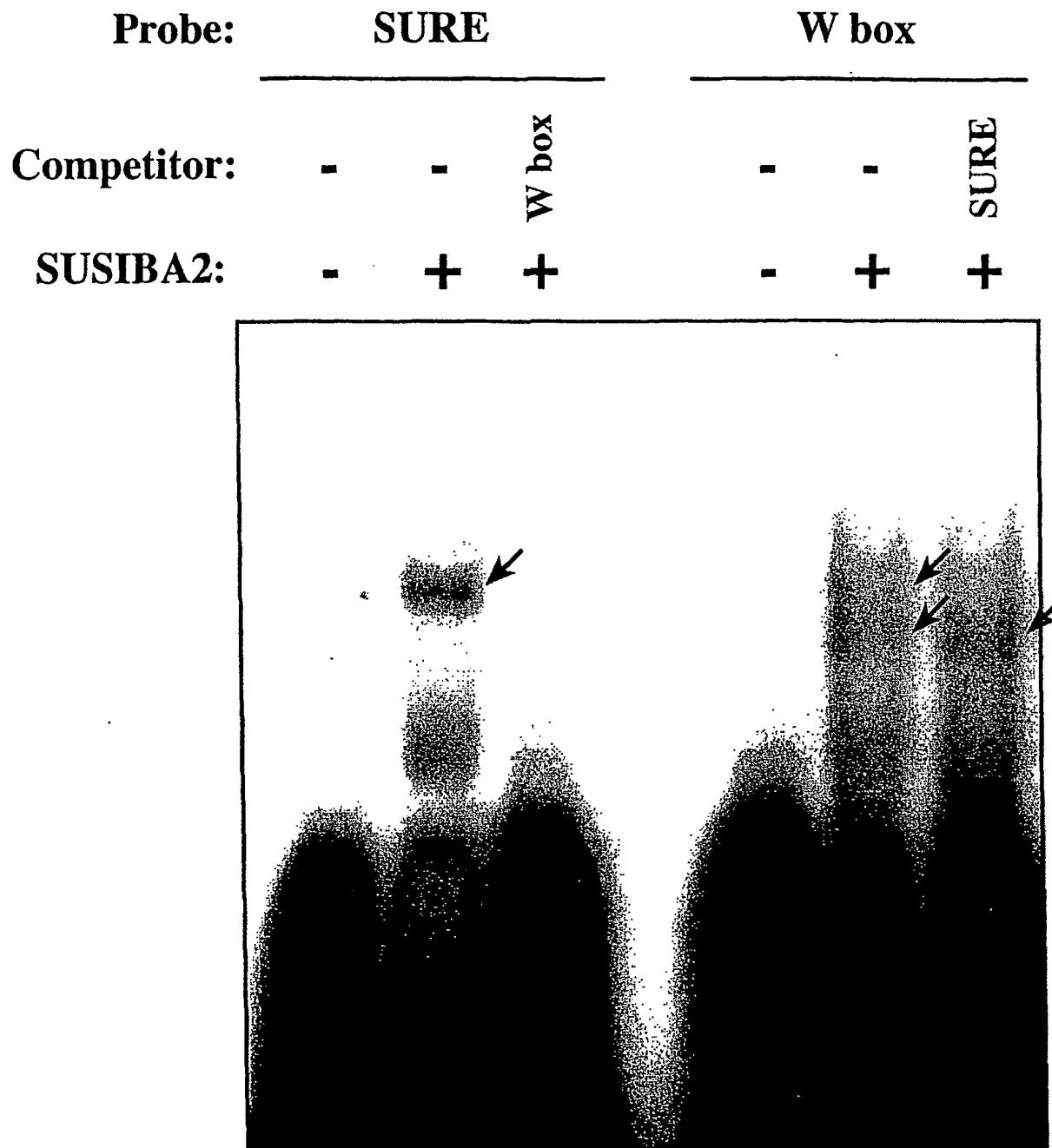
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Figure 6**A**

SP8a probe	-772	CCCTCGTGGAAAGCAAAACTGTGTTCTCGC	-743
		GGGAGCACCTTCGTTGACACAAAGAGCG	
SURE probe	-578	GGAAAACCGAAATACCAAAAAATAATAATAATAAT	-539
		CCTTTGGCTTATGGTTTTATTATTATTATTATT	
W box probe	-411	TCGCTAACCAAGTGAATTCCACGTTCATCATTATT	-376
		AGCGATTGGTCACTGAAGGTGCAAAGTAGTAAATAA	

B

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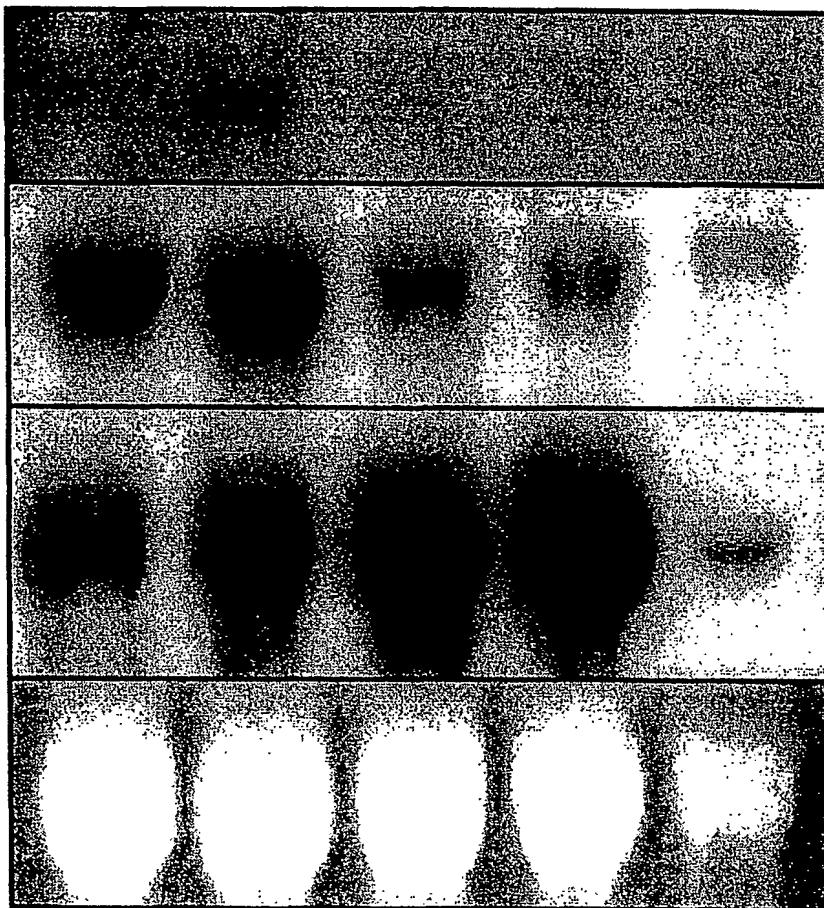
Figure 7

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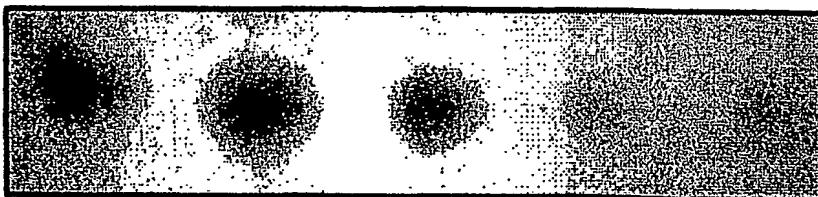
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Figure 8**A**

7 12 17 22 27 (d. a. p.)

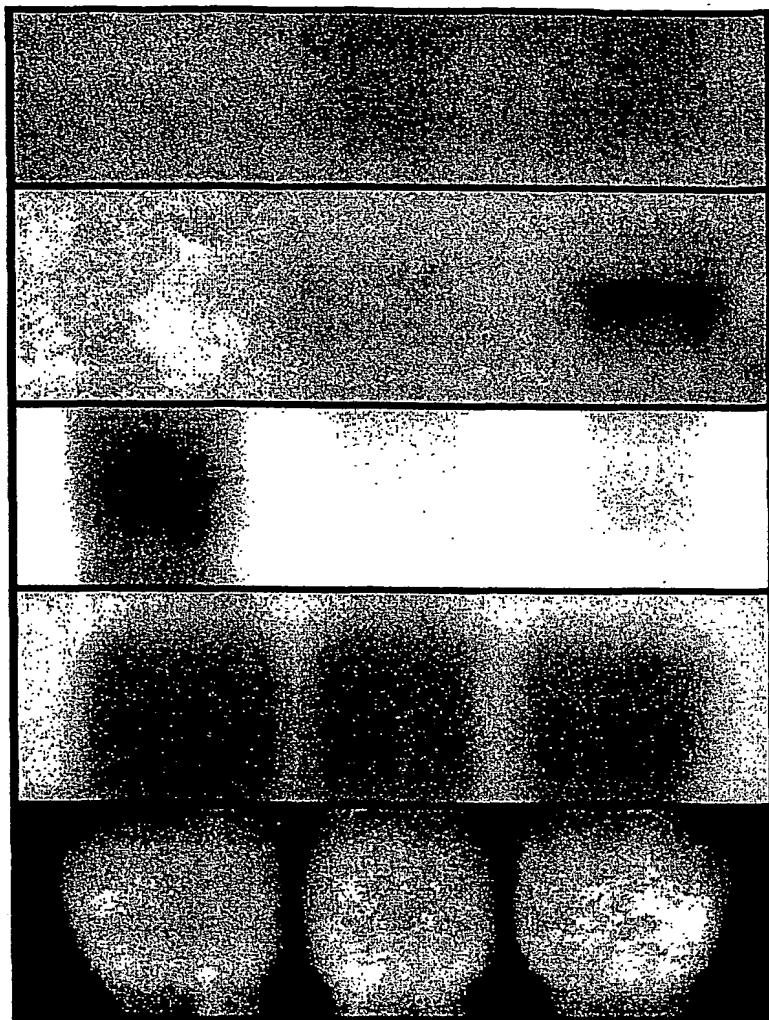
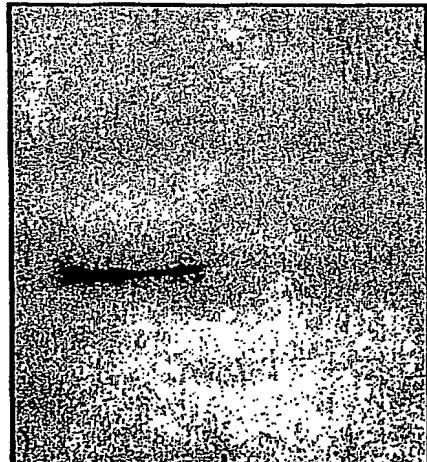
*susiba2**isol**pazl*EtBr-stained
rRNA**B**

7 12 17 22 27 (d. a. p.)



Sucrose

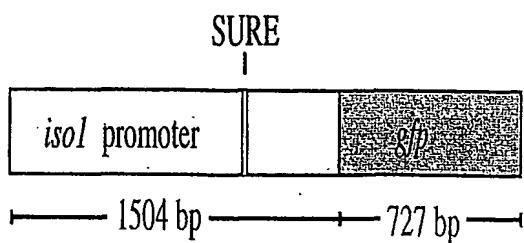
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Figure 9**A** 0 100 200 (mM sucrose)*susiba2**isol**rbcS**rbcL*EtBr-stained
rRNA**B**

Endosperm Leaves

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Figure 10**A***isol::gfp* construct

Decoy

GGAAAACCGAAATACCAAAAAATAATAATAAAAATAATAAT
CCTTTGGCTTATGGTTTTATTATTATTTATTATTA

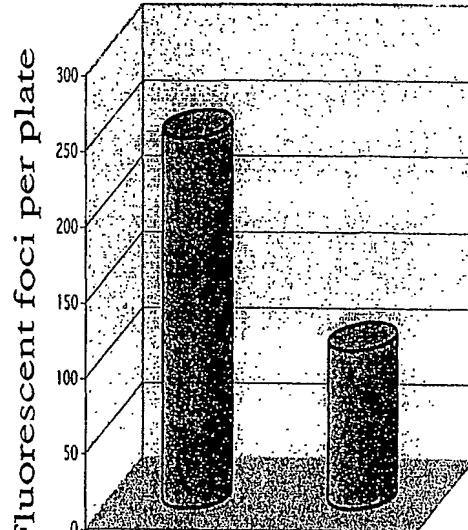
— SURE —

B

- Decoy



+ Decoy

C

- Decoy

+ Decoy

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Figure 11**A**

Residue No. 20 40 60



100 % identity

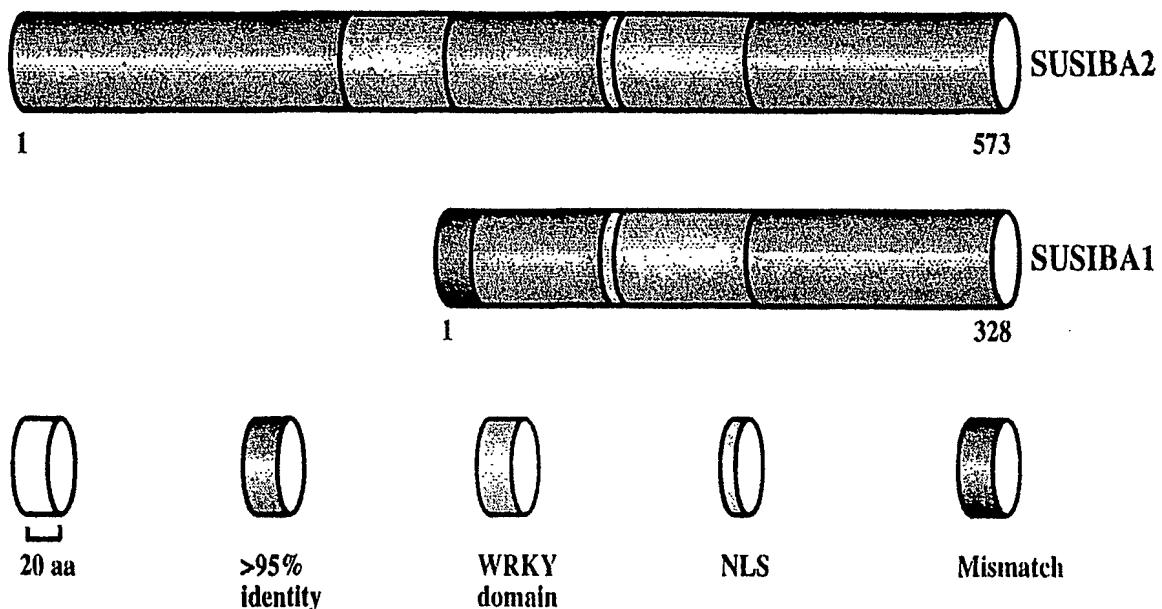
Mismatch

B

SUSIBA2	MSPARLPISRESCLTIPAGFSPSALL	SPVLLTNFKVEPSPTTG	SLGMAAI	EEHKSAHPDM
Rice	MSPARLPISREPCLTIPAGFSPSALL	SPVLLTNFKVEPSPTTG	LSMAAI	ENKSAHPDM
SUSIBA2	LPSPRDKSVRNAHEDRGSRDFEFKPHLNSSSQSI	PAAMS	DLKKHEHSMQNO	SNPSSSS
Rice	LPSPRDKUSGSTHEDEGSRDFEFKPHLNSSSQSI	ASA	NDPKKHE	ASMKNESINTALSSD
SUSIBA2	MMVNEENRPFCSRESSLAVNMS-AQ	QNPVGMVGLTD	SPAEVGTS	POOMNSSD
Rice	MMVNEENRPFCSRESSLAVNMS-SSAP	QVGMVGLTD	SPAEVGTS	ELQMNSSG
SUSIBA2	SENVAEKSADDGYNWRKYGQKHVKGSENPRSY	KC	TPNC	EVKKLLERAVDGLITEVVYK
Rice	SENVAEKSADDGYNWRKYGQKHVKGSENPRSY	KC	TPNC	EVKKLLERSLDGQITEVVYK
SUSIBA2	GRHNHPKPQPNRRLAGGA	VPSNO	GEERYD	GASAA
Rice	GRHNHPKPQPNRRLSAGAVPPI	QGEERYD	GAT	DDKSSNVL
SUSIBA2	SVSDDDDIDAGGGRPYPGDDA	EEED	LESKRRK	MESAGIDAALMGKP
Rice	SVSDDDDIDAGGGRPYPGDDA	EEED	LESKRRK	MESAGIDAALMGKP
SUSIBA2	DILDDGYRWRKYGQKVVKG	NPNP	RSYYKCT	STGCPVRKHVERASHD
Rice	DILDDGYRWRKYGQKVVKG	NPNP	RSYYKCT	STGCPVRKHVERASHD
SUSIBA2	EVPAARNATHEMSAPP	MKNV	VH	DPKSVITTYEGKHNH
Rice	EVPAARNATHEMSAPP	MKNV	VH	DPKSVITTYEGKHNH
SUSIBA2	LGVGISP	NHS	DATNO	QSSGF
Rice	LGVGISP	NHS	DATNO	QSSVS
SUSIBA2	REEKGNEGFTF	ATPM	DHSANLCYS	SAGNLVMGP
Rice	REEKPSEGFTF	ATPM	DHSANLCYS	SAGNLVMGP

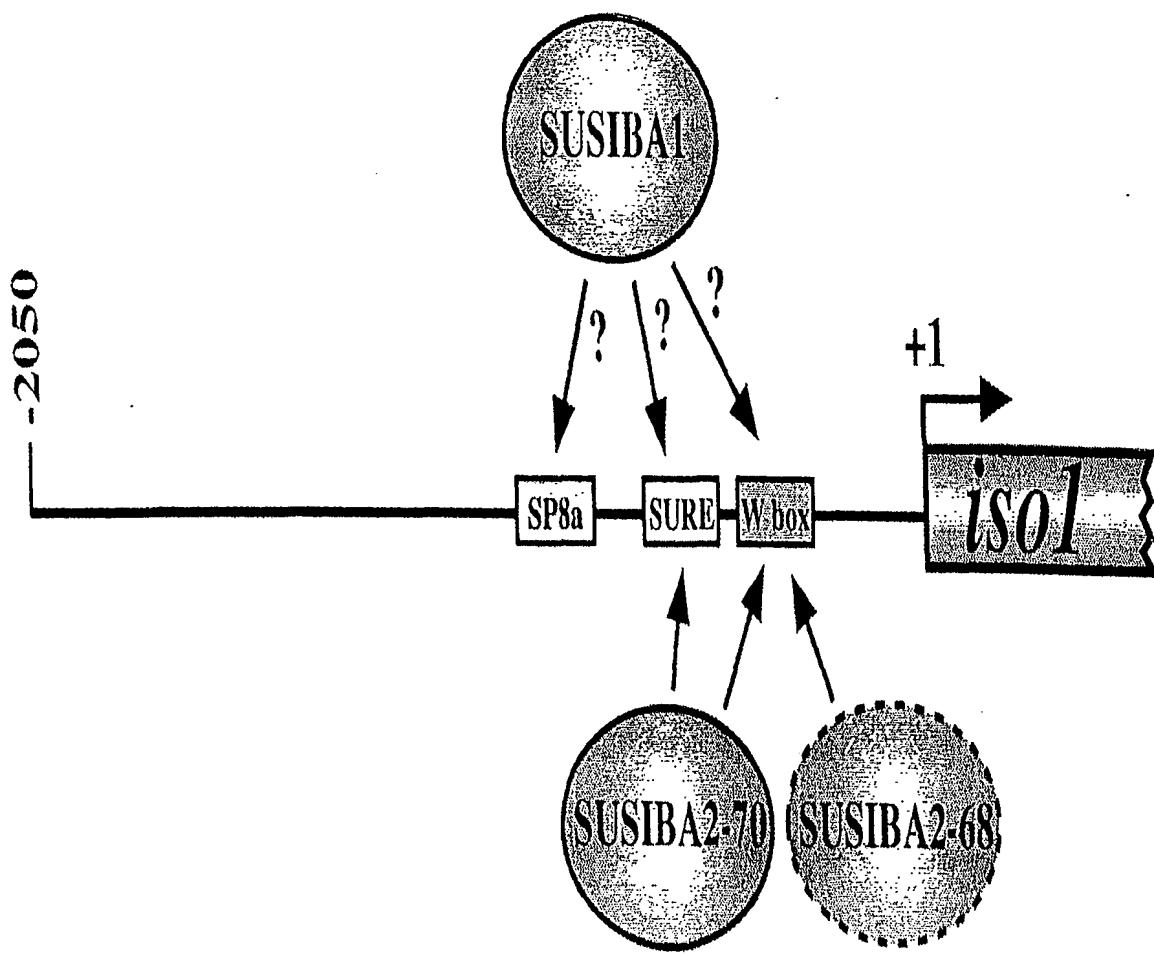
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Figure 12

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Figure 13

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Figure 14

SURE-c	-514	-----AAAAAATAAAAGAAAATGAAATC-----	-494
SURE-b	-568	-----AATACCAAAAAATAA-TAATAAAA-----	-546
SURE-a	-603	-----CCGAAAAAAACTAAGAAAGACCGATG	-578
<i>sbeIIb</i>	-253	-----G-TAATAAAAAA---GG-----G	-240
<i>ssi</i>	-589	----AAATCCTAAAAAAAT-----	-570
<i>agpaseS</i>	-1132	-----TA-AAATAAAAAC-AAAG-----G	-1116
<i>amy</i>	-1375	----GCAGAAGATAAAAAACAA-----	-1356
<i>sbeI</i>	-314	----ACATA-AAATAAAAAA---AG-----G	-297
<i>sus4</i>	-1287	-----AATAAAAGAAGTAGAAAAA-----	-1270
<i>vsp</i>	-759	----AAAGA-AAATAAAAATAAAG-----	-778
<i>PI-II</i>	-548	ATGATAATTA-TTAAACAAAGCAAGT-----	-520
<i>ps20</i>	-172	----AATACTAATAAGAA-TAGAAAAA-----G	-149

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